Amendments to the Claims:

1-29. (Cancelled)

30. (Currently amended) A process for the production of a *Haemophilus influenzae*-specific lipooligosaccharide (LOS) which comprises the steps of:

(a) growing in a culture medium gram-negative bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding ~~comprising~~ an ~~Undecapaprenyl~~ Undecaprenyl-phosphate ~~(UDP)~~ N-acetyl glucosaminyl ~~glucosamine (GlcNAc):Undecapronol GlcNAc-1~~-phosphate transferase (*rfe*) ~~gene~~, and (iii) an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide ~~(*lsgG*) gene product~~ (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by LsgG such that a *H. influenzae*-specific LOS is synthesized by the addition of an acceptor molecule to the terminal heptose molecule; and

(b) recovering the *H. influenzae*-specific LOS from the culture medium.

31. (Previously presented) The process of claim 30, wherein the bacteria are *Escherichia coli*.

32. (Previously presented) The process of claim 31, wherein the bacteria are *Escherichia coli* K-12 strain JM 109.

33. (Previously presented) The process of claim 30, wherein the bacteria are *Salmonella minnesota*.

34. (Previously presented) The process of claim 30, wherein the acceptor molecule is N-acetylglucosamine.

35. (Currently amended) The process of claim 30, wherein the DNA sequence encoding *rfe* ~~gene~~ is from *Haemophilus influenzae*.

36. (Currently amended) The process of claim 30, wherein the DNA sequence encoding ~~comprising~~ a *rfe* ~~gene~~ is part of the gram-negative bacterial genome.

37. (Currently amended) The process of claim 30, wherein the isolated DNA sequence encoding the ~~*lsgG*~~ LsgG is ~~contained~~ comprised in a vector.

38. (Previously presented) The process of claim 30, wherein the bacteria further comprise a glycosyltransferase.

39. (Currently amended) A process for the production of a complex carbohydrate comprising the steps of:

(a) growing in a culture medium gram-negative bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding ~~comprising~~ an Undecaprenyl~~Undecapaprenyl~~ phosphate ~~(UDP)~~ N-acetyl glucosaminyl ~~glucosamine (GleNAc):Undecaprenol GleNAc 1~~ phosphate transferase (*rfe*) ~~gene~~, and (iii) an isolated DNA sequence encoding a liposaccharide-synthesis gene G polypeptide ~~(*lsgG*) gene product~~ (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* ~~gene~~ is regulated by LsgG such that a complex carbohydrate is synthesized by the addition of an acceptor molecule to the heptose molecule; and

(b) recovering the complex carbohydrate from the culture medium.

40. (Previously presented) The process of claim 39, wherein the bacteria are *Escherichia coli*.

41. (Previously presented) The process of claim 40, wherein the bacteria are *Escherichia coli* K-12 strain JM 109.

42. (Previously presented) The process of claim 39, wherein the bacteria are *Salmonella minnesota*.

43. (Previously presented) The process of claim 39, wherein the acceptor molecule is N-acetylglucosamine.

44. (Currently amended) The process of claim 39, wherein the DNA sequence encoding *rfe* ~~gene~~ is from *Haemophilus influenzae*.

45. (Currently amended) The process of claim 39, wherein the DNA sequence encoding ~~comprising~~ a *rfe* ~~gene~~ is part of the gram-negative bacterial genome.

46. (Currently amended) The process of claim 39, wherein the isolated DNA sequence encoding LsgG ~~comprising the *lsgG*~~ is contained in a vector.

47. (Previously presented) The process of claim 39, wherein the bacteria further comprise a glycosyltransferase.

48. (Currently amended) A method of modifying a terminal heptose of a lipopolysaccharide (LPS) or lipooligosaccharide (LOS) core structure of a gram-negative bacterial species comprising a polynucleotide encoding ~~containing~~ an Undecaprenyl~~Undecapaprenyl~~ phosphate ~~(UDP)~~ N-acetyl glucosaminyl ~~glucosamine (GlcNAc):Undecaprenol GlcNAc 1~~ phosphate transferase (*rfe*), wherein ~~gene comprising regulating~~ the polynucleotide encoding *rfe* is regulated by ~~gene with a protein encoded by an isolated~~ lipooligosaccharide-synthesis gene G polypeptide (LsgG) ~~(*lsgG*)~~ ~~gene~~ from *Haemophilus influenzae* such that an N-acetyl glucosamine is added onto the terminal heptose.

49. (Previously presented) The method of claim 48 wherein the bacteria are *Escherichia coli*.

50. (Previously presented) The method of claim 49, wherein the bacteria are *Escherichia coli* K-12 strain JM 109.

51. (Previously presented) The method of claim 48, wherein the bacteria are *Salmonella minnesota*.

52. (Currently amended) The method of claim 48, wherein the polynucleotide encoding *rfe* ~~gene~~ is from *Haemophilus influenzae*.

53. (Currently amended) The method of claim 48, wherein the polynucleotide encoding *rfe* ~~gene~~ is part of the gram-negative bacterial genome.

54. (Currently amended) The method of claim 48, wherein ~~the~~ a polynucleotide encoding the LsgG ~~isolated *lsgG* gene~~ is comprised ~~contained~~ in a vector.

55. (Previously presented) The method of claim 48, wherein the bacteria further comprise a glycosyltransferase.